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Applicant(s): Raghuram Kalluri

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For: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF
USE THEREOF

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Although a Notice to Comply with Sequence Rules 37 C.F.R. §§1.821-1.825 has not been received in our offices, transmitted herewith is a copy of the "Sequence Listing" (sheets 1/9 through 9/9) in paper form for the above-identified patent application as required by 37 C.F.R. §1.821(c) and a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicant's Attorney hereby states that the content of the "Sequence Listing" in paper form and the computer readable form of the "Sequence Listing" are the same and, as required by 37 C.F.R. §1.821(g), also states that the submission includes no new matter.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By 

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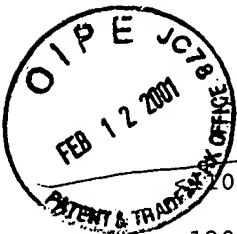
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Date: *February 8, 2001*

6/A



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SEQUENCE LISTING

FEB 20 2001

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<120> ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS
AND METHODS OF USE THEREOF

TECH CENTER 1600/2900

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<140> US 09/543,371

<141> 2000-04-04

<150> US 09/335,224

<151> 1999-06-17

<150> US 60/089,689

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<160> 18

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gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct 96
Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
20 25 30

ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc 144
Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
35 40 45

acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc 192
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
50 55 60

tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg 240
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65 70 75 80

tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc	288
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile	
85 90 95	
acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag	336
Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu	
100 105 110	
gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca	384
Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro	
115 120 125	
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Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val	
130 135 140	
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Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser	
145 150 155 160	
ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt	528
Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys	
165 170 175	
cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg	576
His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp	
180 185 190	
ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc	624
Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser	
195 200 205	
acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa gtc	672
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<213> Homo sapiens

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35 40 45	
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe	
50 55 60	
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser	
65 70 75 80	
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile	
85 90 95	

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145					150					155					160
Pro	Gly	Ser	Cys	Leu	Glu	Glu	Phe	Arg	Ser	Ala	Pro	Phe	Ile	Glu	Cys
			165						170					175	
His	Gly	Arg	Gly	Thr	Cys	Asn	Tyr	Tyr	Ala	Asn	Ala	Tyr	Ser	Phe	Trp
			180					185					190		
Leu	Ala	Thr	Ile	Glu	Arg	Ser	Glu	Met	Phe	Lys	Lys	Pro	Thr	Pro	Ser
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48

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ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu 35 40 45	144
gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys 50 55 60	192
aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr 65 70 75 80	240
tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp 85 90 95	288
gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala 100 105 110	336
atc gcc atc gcg gtc cac agt cag gat gtc tcc atc cca cac tgc cca Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro 115 120 125	384
gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc ctc atg cac acg Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr 130 135 140	432
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tgt cta gag gac ttc cgc gcc aca cca ttc atc gaa tgc aat gga ggc Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly 165 170 175	528
cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr 180 185 190	576
acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu 195 200 205	624
aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met 210 215 220	672
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<213> Homo sapiens

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35 40 45
Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
50 55 60
Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
65 70 75 80
Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
85 90 95
Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
100 105 110
Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
115 120 125
Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
130 135 140
Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
145 150 155 160
Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
165 170 175
Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
180 185 190
Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
195 200 205
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Lys Asn Leu
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<213> Artificial Sequence

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<223> pET22b(+) forward oligonucleotide primer for
Canstatin

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27

<210> 8

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<212> DNA

<213> Artificial Sequence

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<223> pET22b(+) reverse oligonucleotide primer for
Canstatin

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 Thr Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile
 20 25 30

cct tca tgt cca gag ggg aca gtg cca ctc tac agt ggg ttt tct ttt 144
 Pro Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe
 35 40 45

ctt ttt gta caa gga aat caa cga gcc cac gga caa gac ctt gga act 192
 Leu Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr
 50 55 60

ctt ggc agc tgc ctg cag cga ttt acc aca atg cca ttc tta ttc tgc 240
 Leu Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys
 65 70 75

aat gtc aat gat gta tgt aat ttt gca tct cga aat gat tat tca tac 288
 Asn Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr
 80 85 90 95

tgg ctg tca aca cca gct ctg atg cca atg aac atg gct ccc att act 336
 Trp Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr
 100 105 110

ggc aga gcc ctt gag cct tat ata agc aga tgc act gtt tgt gaa ggt 384
 Gly Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly
 115 120 125

cct gcg atc gcc ata gcc gtt cac agc caa acc act gac att cct cca 432
 Pro Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro
 130 135 140

tgt cct cac ggc tgg att tct ctc tgg aaa gga ttt tca ttc atc atg	480
Cys Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met	
145 150 155	
ttc aca agt gca ggt tct gag ggc acc ggg caa gca ctg gcc tcc cct	528
Phe Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro	
160 165 170 175	
ggc tcc tgc ctg gaa gaa ttc cga gcc agc cca ttt cta gaa tgt cat	576
Gly Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His	
180 185 190	
gga aga gga acg tgc aac tac tat tca aat tcc tac agt ttc tgg ctg	624
Gly Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu	
195 200 205	
gct tca tta aac cca gaa aga atg ttc aga aag cct att cca tca act	672
Ala Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr	
210 215 220	
gtg aaa gct ggg gaa tta gaa aaa ata ata agt cgc tgt cag gtg tgc	720
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225 230 235	
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Met Lys Lys Arg His	
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 <213> Homo sapiens

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<221> PEPTIDE
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 Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
 35 40 45
 Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
 50 55 60
 Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
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Leu	Ser	Thr	Pro	Ala	Leu	Met	Pro	Met	Asn	Met	Ala	Pro	Ile	Thr	Gly
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Arg	Ala	Leu	Glu	Pro	Tyr	Ile	Ser	Arg	Cys	Thr	Val	Cys	Glu	Gly	Pro
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Ala	Ile	Ala	Ile	Ala	Val	His	Ser	Gln	Thr	Thr	Asp	Ile	Pro	Pro	Cys
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Pro	His	Gly	Trp	Ile	Ser	Leu	Trp	Lys	Gly	Phe	Ser	Phe	Ile	Met	Phe
145					150					155				160	
Thr	Ser	Ala	Gly	Ser	Glu	Gly	Thr	Gly	Gln	Ala	Leu	Ala	Ser	Pro	Gly
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Ser	Cys	Leu	Glu	Glu	Phe	Arg	Ala	Ser	Pro	Phe	Leu	Glu	Cys	His	Gly
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Arg	Gly	Thr	Cys	Asn	Tyr	Tyr	Ser	Asn	Ser	Tyr	Ser	Phe	Trp	Leu	Ala
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Ser	Leu	Asn	Pro	Glu	Arg	Met	Phe	Arg	Lys	Pro	Ile	Pro	Ser	Thr	Val
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Lys	Ala	Gly	Glu	Leu	Glu	Lys	Ile	Ile	Ser	Arg	Cys	Gln	Val	Cys	Met
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<213> Artificial Sequence

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<223> Additional vector sequence added to protein

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<210> 15

<211> 28

<212> DNA

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<223> pPICZaA forward oligonucleotide primer for
 Arresten

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<212> DNA

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<223> pPICZaA reverse oligonucleotide primer for
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<212> DNA

<213> Artificial Sequence

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 Canstatin

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<210> 18

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<212> DNA

<213> Artificial Sequence

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<223> pPICZaA reverse oligonucleotide primer for
 Canstatin

<400> 18

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32